

*Seq A1* >

SEQUENCE LISTING

<110> PODBIELSKI, ANDREAS

<120> COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES

<130> P06628US0/BAS

<140> 00/000,000

<141> 2000-01-31

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 2274

<212> DNA

<213> *Streptococcus pyogenes*

<400> 1

atgaaaaaaaaa caaggtttcc aaataagctt aatactctta atactcaaag ggtattaagt 60  
aaaaaactcaa aacgatttac tgtcacttta gtggagtc tttaatgat cttcgcttg 120  
gttaacttcca tggttggtgc taagactgtt tttggtttag tagaattcctc gacgccaaac 180  
gcaataaaatc cagattcaag ttccgaaatac agatggatag gatatgaatc ttatgtaaga 240  
ggcattccat attataaaaca gtttagagta gcacacgatt taagggttaa cttagaagga 300  
agtagaagtt atcaagtttta ttgctttaat ttaaaagaaag catttcctct cggatcagat 360  
agttagtgtta aaaagtggta taaaaaaacat gatggaatct ctacaaaatt tgaagattat 420  
gcatgatgagcc ctagaattac gggagatgag ctaaatcaga agttacgagc tgttatgtat 480  
aatggacatc cacaaaatgc caatggtatt atggaaggct tggAACCCttt gaatgctatc 540

agagttacac aagaggcggt atggtaactat tctgataatg ctcctatttc taatccagat 600  
gaaagttta aaagggagtc agaaagtaac ttggtagta cttctcaatt atctttgatg 660  
cgtcaagctt tgaagcaact gattgatccg aatttggcaa ctaaaatgcc aaaacaagtt 720  
ccggatgatt ttcagctaag tatttttag tctgaggaca agggagataa atataataaa 780  
ggataccaaa atcttttag tggtggtta gttcctacta aaccaccaac tccaggagac 840  
ccaccaatgc ctccaaatca acctcaaacg acttcagtac ttattagaaa gtatgctata 900  
ggtgattact ctaaattgct tgaaggtgca acattacagt tgacagggga taacgtgaat 960  
agtttcaag cgagagtgtt tagcagtaat gatattggag aaagaattga actatcagat 1020  
ggaacttata cttaactga attgaattct ccagctggtt atagtatcgc agagccaatc 1080  
acttttaagg ttgaagctgg caaagtgtat actattattg atggaaaaca gattgaaaat 1140  
cccaataaag agatagtaga gccttactca gtagaagcat ataatgattt tgaagaattt 1200  
agcgtttaa ctacacaaaa ctatgcaaaa ttttattatg caaaaaataa aaatggaagt 1260  
tcacagggtt tctattgctt taatgcagat ctaaaatctc caccagactc tgaagatggt 1320  
gggaaaacaa tgactccaga ctttacaaca ggagaagtaa aatacactca tattgcaggt 1380  
cgtgacctct ttaaatatac tgtgaaacca agagataccg atcctgacac tttcttaaaa 1440  
catatcaaaa aagtaattga gaagggttac agggaaaaag gacaagctat tgagtatagt 1500  
ggtcttaactg agacacaatt gcgtgcggct actcagttag caatatatta tttcactgat 1560  
agtgctgaat tagataagga taaactaaaa gactatcatg gttttggaga catgaatgat 1620  
agtactttag cagttgctaa aatccttcta gaatacgctc aagatagtaa tcctccacag 1680  
ctaactgacc ttgatttctt tattccgaat aacaataaat atcaatctct tattggaact 1740  
cagtggcatc cagaagattt agttgatatt attcgatgg aagataaaaa agaagttata 1800  
cctgtaactc ataatttaac attgagaaaa acggtgactg gtttagctgg tgacagaact 1860  
aaagatttcc attttgaat tgaattaaaa aataataagc aagaattgtt ttctcaaact 1920  
gttaaaacag ataaaacaaa cctcgaattt aaagatggta aagcaaccat taatttaaaa 1980  
catggggaaa gtttaacact tcaaggtta ccagaagggtt attcttacct tgtcaaagaa 2040  
acagattctg aaggctataa gtttaaagtt aatagccaag aagtagcaaa tgctacagtt 2100  
tcaaaaacag gaataacaag tgatgagaca cttgctttg aaaataataa aggcctgtt 2160  
gttcctacag gagttgatca aaagatcaat ggctatctag ctttgatagt tatcgctggt 2220

atcagttgg ggatctgggg aattcacacg ataaggataa gaaaacatga ctag 2274

<210> 2

<211> 757

<212> PRT

<213> **Streptococcus pyogenes**

<400> 2

Met Lys Lys Thr Arg Phe Pro Asn Lys Leu Asn Thr Leu Asn Thr Gln

1 5 10 15

Arg Val Leu Ser Lys Asn Ser Lys Arg Phe Thr Val Thr Leu Val Gly

20 25 30

Val Phe Leu Met Ile Phe Ala Leu Val Thr Ser Met Val Gly Ala Lys

35 40 45

Thr Val Phe Gly Leu Val Glu Ser Ser Thr Pro Asn Ala Ile Asn Pro

50 55 60

Asp Ser Ser Ser Glu Tyr Arg Trp Tyr Gly Tyr Glu Ser Tyr Val Arg

65 70 75 80

Gly His Pro Tyr Tyr Lys Gln Phe Arg Val Ala His Asp Leu Arg Val

85 90 95

Asn Leu Glu Gly Ser Arg Ser Tyr Gln Val Tyr Cys Phe Asn Leu Lys

100 105 110

Lys Ala Phe Pro Leu Gly Ser Asp Ser Ser Val Lys Lys Trp Tyr Lys

115

120

125

Lys His Asp Gly Ile Ser Thr Lys Phe Glu Asp Tyr Ala Met Ser Pro

130

135

140

Arg Ile Thr Gly Asp Glu Leu Asn Gln Lys Leu Arg Ala Val Met Tyr

145

150

155

160

Asn Gly His Pro Gln Asn Ala Asn Gly Ile Met Glu Gly Leu Glu Pro

165

170

175

Leu Asn Ala Ile Arg Val Thr Gln Glu Ala Val Trp Tyr Tyr Ser Asp

180

185

190

Asn Ala Pro Ile Ser Asn Pro Asp Glu Ser Phe Lys Arg Glu Ser Glu

195

200

205

Ser Asn Leu Val Ser Thr Ser Gln Leu Ser Leu Met Arg Gln Ala Leu

210

215

220

Lys Gln Leu Ile Asp Pro Asn Leu Ala Thr Lys Met Pro Lys Gln Val

225

230

235

240

Pro Asp Asp Phe Gln Leu Ser Ile Phe Glu Ser Glu Asp Lys Gly Asp

245

250

255

Lys Tyr Asn Lys Gly Tyr Gln Asn Leu Leu Ser Gly Gly Leu Val Pro

260 265 270

Thr Lys Pro Pro Thr Pro Gly Asp Pro Pro Met Pro Pro Asn Gln Pro

275 280 285

Gln Thr Thr Ser Val Leu Ile Arg Lys Tyr Ala Ile Gly Asp Tyr Ser

290 295 300

Lys Leu Leu Glu Gly Ala Thr Leu Gln Leu Thr Gly Asp Asn Val Asn

305 310 315 320

Ser Phe Gln Ala Arg Val Phe Ser Ser Asn Asp Ile Gly Glu Arg Ile

325 330 335

Glu Leu Ser Asp Gly Thr Tyr Thr Leu Thr Glu Leu Asn Ser Pro Ala

340 345 350

Gly Tyr Ser Ile Ala Glu Pro Ile Thr Phe Lys Val Glu Ala Gly Lys

355 360 365

Val Tyr Thr Ile Ile Asp Gly Lys Gln Ile Glu Asn Pro Asn Lys Glu

370 375 380

Ile Val Glu Pro Tyr Ser Val Glu Ala Tyr Asn Asp Phe Glu Glu Phe

385 390 395 400

Ser Val Leu Thr Thr Gln Asn Tyr Ala Lys Phe Tyr Tyr Ala Lys Asn

405

410

415

Lys Asn Gly Ser Ser Gln Val Val Tyr Cys Phe Asn Ala Asp Leu Lys

420

425

430

Ser Pro Pro Asp Ser Glu Asp Gly Gly Lys Thr Met Thr Pro Asp Phe

435

440

445

Thr Thr Gly Glu Val Lys Tyr Thr His Ile Ala Gly Arg Asp Leu Phe

450

455

460

Lys Tyr Thr Val Lys Pro Arg Asp Thr Asp Pro Asp Thr Phe Leu Lys

465

470

475

480

His Ile Lys Lys Val Ile Glu Lys Gly Tyr Arg Glu Lys Gly Gln Ala

485

490

495

Ile Glu Tyr Ser Gly Leu Thr Glu Thr Gln Leu Arg Ala Ala Thr Gln

500

505

510

Leu Ala Ile Tyr Tyr Phe Thr Asp Ser Ala Glu Leu Asp Lys Asp Lys

515

520

525

Leu Lys Asp Tyr His Gly Phe Gly Asp Met Asn Asp Ser Thr Leu Ala

530

535

540

Val Ala Lys Ile Leu Val Glu Tyr Ala Gln Asp Ser Asn Pro Pro Gln

545

550

555

560

Leu Thr Asp Leu Asp Phe Phe Ile Pro Asn Asn Asn Lys Tyr Gln Ser

565

570

575

Leu Ile Gly Thr Gln Trp His Pro Glu Asp Leu Val Asp Ile Ile Arg

580

585

590

Met Glu Asp Lys Lys Glu Val Ile Pro Val Thr His Asn Leu Thr Leu

595

600

605

Arg Lys Thr Val Thr Gly Leu Ala Gly Asp Arg Thr Lys Asp Phe His

610

615

620

Phe Glu Ile Glu Leu Lys Asn Asn Lys Gln Glu Leu Leu Ser Gln Thr

625

630

635

640

Val Lys Thr Asp Lys Thr Asn Leu Glu Phe Lys Asp Gly Lys Ala Thr

645

650

655

Ile Asn Leu Lys His Gly Glu Ser Leu Thr Leu Gln Gly Leu Pro Glu

660

665

670

Gly Tyr Ser Tyr Leu Val Lys Glu Thr Asp Ser Glu Gly Tyr Lys Val

675

680

685

Lys Val Asn Ser Gln Glu Val Ala Asn Ala Thr Val Ser Lys Thr Gly

690

695

700

Ile Thr Ser Asp Glu Thr Leu Ala Phe Glu Asn Asn Lys Glu Pro Val

705

710

715

720

Val Pro Thr Gly Val Asp Gln Lys Ile Asn Gly Tyr Leu Ala Leu Ile

725

730

735

Val Ile Ala Gly Ile Ser Leu Gly Ile Trp Gly Ile His Thr Ile Arg

740

745

750

Ile Arg Lys His Asp

755

<210> 3

<211> 2229

<212> DNA

<213> *Streptococcus pyogenes*

<400> 3

ttgcaaaaaga gggataaaac caattatgga agcgctaaca acaaacgacg acaaacgacg 60

atcggattac tgaaagtatt tttgacgttt gtagctctga taggaatagt agggtttct 120

atcagagcgt tcggagctga agaacaatca gtaccaaata gacaaagctc aattcaagat 180

tatccgtggt atggctatga ttcttacccct aaaggctacc cagactatag tccgttaaag 240

acttaccata attaaaaagt aaatttagag ggaagtaagg attatcaagc atactgcttt 300

aatttaacaa aacattttcc atccaagtca gatagtgtta gatcacaatg gtataaaaaa 360

cttgaaggaa ctaatgaaaa ctttatcaag ttagcagata aaccaagaat agaagacgga 420

cagttacaac aaaatatatt gaggattctc tataatggat atcctaataa tcgtaatggg 480

ataatgaaag ggatagatcc tctaaacgct attttagtga ctcaaaatgc tatttggat 540

actgattcag ctcaaattaa tccggatgaa agtttaaaa cagaagctcg aagtaatgg 600

atataatgacc agcaggttagg cttaatgcga aaagctttaa aagaactaat tgatccaaac 660  
ttagggtcaa aatattcgaa taaaactcca tcaggttatac ggttaaatgt atttgaatct 720  
catgataagc ctttccaaaaa tcttttgagt gctgagttatg ttccggatac tcccccaaaa 780  
ccaggagaag agcctccggc taaaactgaa aaaacatcag tcattatcag aaaatatgct 840  
gaaggtgact ctaaacttct agagggagca accttaaagc tttctcaaatt tgaaggaagt 900  
ggtttcaag aaaaagactt tcaaagtaat agtttaggag aaactgtcga attaccaaatt 960  
gggacttata ccttaacaga aacatcatct ccagatggat ataaaattgc ggagccgatt 1020  
aagtttagag tagagaataa aaaaagtattt atcgccaaa aagatggtc tcaagtggaa 1080  
aatccaaaca aagaagttagc agagccatac tcagtgaaag cgtataatga ctatggat 1140  
gaagaagtac tctcgggtt tactccatac ggaaaattct attacgctac aaataaggat 1200  
aaaagttcac aagttgtcta ctgcttcaat gctgatttac actcaccacc tgactcatat 1260  
gatagtggtg agactataaa tccagatact agtacgatga aagaagtcaa gtacacacat 1320  
acggcaggtt gtgacttgg taaatatgct ctaagaccga gagatacaaa tccagaagac 1380  
ttcttaaagc acattaaaaa agtaattgaa aaaggctaca agaaaaaaagg tgatagttat 1440  
aatggattaa cagaaacaca gttcgcgcg gctactcagc ttgctatcta ttatttaca 1500  
gacagtgctg actaaaaac cttaaaaact tataacaatg ggaaaggta ccatggattt 1560  
gaatctatgg atgaaaaaaac cctagctgtc aaaaaagaat taattactta tgctcaaaat 1620  
ggcagtgcgc ctcactaac aaatcttgc ttcttcgtac ctaataatag caaagaccaa 1680  
tctcttattt ggacagaatg ccatccagat gattgggtt acgtgattcg tatggaagat 1740  
aaaaagcaag aagttattcc agtaactcac agtttgacag tgaaaaaaac agtagtcggt 1800  
gagttggag ataaaactaa aggcttccaa tttgaacttg agttgaaaga taaaactgga 1860  
cagcctattt ttaacactct aaaaactaat aatcaagatt tagtagctaa agatggaaa 1920  
tattcattt atctaaagca tggtgacacc ataagaatag aaggattacc gacgggatat 1980  
tcttatactc tgaaagaggc tgaagcttgc gattatatac taaccgttgc taacaaagtt 2040  
agtcaagaag cgcagtcagt aggttaaggat ataacagaag acaaaaaaagt cactttgaa 2100  
aaccgaaaag atcttgcggc accaactggt ttgacaacag atggggctat ctatcttgg 2160  
ttgttatttac ttgttccact tgggttattt gttggctat ttgggtcgtaa agggtaaaa 2220  
aatgactaa

2229

<210> 4

<211> 742

<212> PRT

<213> **Streptococcus pyogenes**

<400> 4

Met Gln Lys Arg Asp Lys Thr Asn Tyr Gly Ser Ala Asn Asn Lys Arg

1 5 10 15

Arg Gln Thr Thr Ile Gly Leu Leu Lys Val Phe Leu Thr Phe Val Ala

20 25 30

Leu Ile Gly Ile Val Gly Phe Ser Ile Arg Ala Phe Gly Ala Glu Glu

35 40 45

Gln Ser Val Pro Asn Arg Gln Ser Ser Ile Gln Asp Tyr Pro Trp Tyr

50 55 60

Gly Tyr Asp Ser Tyr Pro Lys Gly Tyr Pro Asp Tyr Ser Pro Leu Lys

65 70 75 80

Thr Tyr His Asn Leu Lys Val Asn Leu Glu Gly Ser Lys Asp Tyr Gln

85 90 95

Ala Tyr Cys Phe Asn Leu Thr Lys His Phe Pro Ser Lys Ser Asp Ser

100 105 110

Val Arg Ser Gln Trp Tyr Lys Lys Leu Glu Gly Thr Asn Glu Asn Phe

115 120 125

Ile Lys Leu Ala Asp Lys Pro Arg Ile Glu Asp Gly Gln Leu Gln Gln

130 135 140

Asn Ile Leu Arg Ile Leu Tyr Asn Gly Tyr Pro Asn Asn Arg Asn Gly

145 150 155 160

Ile Met Lys Gly Ile Asp Pro Leu Asn Ala Ile Leu Val Thr Gln Asn

165 170 175

Ala Ile Trp Tyr Thr Asp Ser Ala Gln Ile Asn Pro Asp Glu Ser Phe

180 185 190

Lys Thr Glu Ala Arg Ser Asn Gly Ile Asn Asp Gln Gln Leu Gly Leu

195 200 205

Met Arg Lys Ala Leu Lys Glu Leu Ile Asp Pro Asn Leu Gly Ser Lys

210 215 220

Tyr Ser Asn Lys Thr Pro Ser Gly Tyr Arg Leu Asn Val Phe Glu Ser

225 230 235 240

His Asp Lys Pro Phe Gln Asn Leu Leu Ser Ala Glu Tyr Val Pro Asp

245 250 255

Thr Pro Pro Lys Pro Gly Glu Glu Pro Pro Ala Lys Thr Glu Lys Thr

260

265

270

Ser Val Ile Ile Arg Lys Tyr Ala Glu Gly Asp Ser Lys Leu Leu Glu

275

280

285

Gly Ala Thr Leu Lys Leu Ser Gln Ile Glu Gly Ser Gly Phe Gln Glu

290

295

300

Lys Asp Phe Gln Ser Asn Ser Leu Gly Glu Thr Val Glu Leu Pro Asn

305

310

315

320

Gly Thr Tyr Thr Leu Thr Glu Thr Ser Ser Pro Asp Gly Tyr Lys Ile

325

330

335

Ala Glu Pro Ile Lys Phe Arg Val Glu Asn Lys Lys Val Phe Ile Val

340

345

350

Gln Lys Asp Gly Ser Gln Val Glu Asn Pro Asn Lys Glu Val Ala Glu

355

360

365

Pro Tyr Ser Val Glu Ala Tyr Asn Asp Phe Met Asp Glu Glu Val Leu

370

375

380

Ser Gly Phe Thr Pro Tyr Gly Lys Phe Tyr Tyr Ala Thr Asn Lys Asp

385

390

395

400

Lys Ser Ser Gln Val Val Tyr Cys Phe Asn Ala Asp Leu His Ser Pro

405

410

415

Pro Asp Ser Tyr Asp Ser Gly Glu Thr Ile Asn Pro Asp Thr Ser Thr

420

425

430

Met Lys Glu Val Lys Tyr Thr His Thr Ala Gly Ser Asp Leu Phe Lys

435

440

445

Tyr Ala Leu Arg Pro Arg Asp Thr Asn Pro Glu Asp Phe Leu Lys His

450

455

460

Ile Lys Lys Val Ile Glu Lys Gly Tyr Lys Lys Lys Gly Asp Ser Tyr

465

470

475

480

Asn Gly Leu Thr Glu Thr Gln Phe Arg Ala Ala Thr Gln Leu Ala Ile

485

490

495

Tyr Tyr Phe Thr Asp Ser Ala Asp Leu Lys Thr Leu Lys Thr Tyr Asn

500

505

510

Asn Gly Lys Gly Tyr His Gly Phe Glu Ser Met Asp Glu Lys Thr Leu

515

520

525

Ala Val Thr Lys Glu Leu Ile Thr Tyr Ala Gln Asn Gly Ser Ala Pro

530

535

540

Gln Leu Thr Asn Leu Asp Phe Phe Val Pro Asn Asn Ser Lys Asp Gln

545

550

555

560

Ser Leu Ile Gly Thr Glu Cys His Pro Asp Asp Leu Val Asp Val Ile  
565 570 575

Arg Met Glu Asp Lys Lys Gln Glu Val Ile Pro Val Thr His Ser Leu  
580 585 590

Thr Val Lys Lys Thr Val Val Asp Glu Leu Gly Asp Lys Thr Lys Gly  
595 600 605

Phe Gln Phe Glu Leu Glu Leu Lys Asp Lys Thr Gly Gln Pro Ile Val  
610 615 620

Asn Thr Leu Lys Thr Asn Asn Gln Asp Leu Val Ala Lys Asp Gly Lys  
625 630 635 640

Tyr Ser Phe Asn Leu Lys His Gly Asp Thr Ile Arg Ile Glu Gly Leu  
645 650 655

Pro Thr Gly Tyr Ser Tyr Thr Leu Lys Glu Ala Glu Ala Lys Asp Tyr  
660 665 670

Ile Val Thr Val Asp Asn Lys Val Ser Gln Glu Ala Gln Ser Val Gly  
675 680 685

Lys Asp Ile Thr Glu Asp Lys Lys Val Thr Phe Glu Asn Arg Lys Asp  
690 695 700

Leu Val Pro Pro Thr Gly Leu Thr Thr Asp Gly Ala Ile Tyr Leu Trp

705

710

715

720

Leu Leu Leu Leu Val Pro Leu Gly Leu Leu Val Trp Leu Phe Gly Arg

725

730

735

Lys Gly Leu Lys Asn Asp

740